# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 19:50:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524766.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524766.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 19:50:00 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524766.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 884,893 |
| Mapped reads | 816,078 / 92.22% |
| Unmapped reads | 68,815 / 7.78% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,793 / 0.43% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 20,081 / 2.27% |
| Duplication rate | 1.8% |
| Clipped reads | 817,646 / 92.4% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,248,605 / 25.82% |
| Number/percentage of C's | 9,057,786 / 19.09% |
| Number/percentage of T's | 15,106,948 / 31.84% |
| Number/percentage of G's | 11,026,851 / 23.24% |
| Number/percentage of N's | 903 / 0% |
| GC Percentage | 42.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0153 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1735 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.19 |

## 2.5. Mismatches and indels

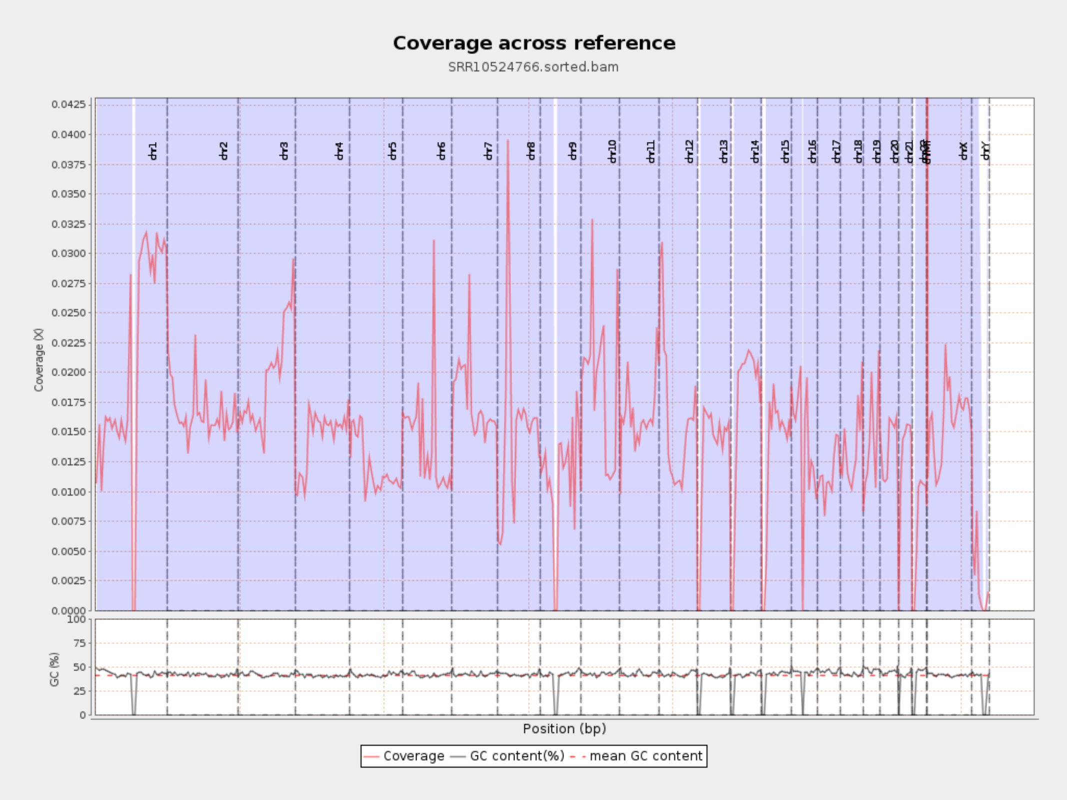
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 236,217 |
| Insertions | 3,363 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 10,005 |
| Mapped reads with at least one deletion | 1.22% |
| Homopolymer indels | 43.3% |

## 2.6. Chromosome stats

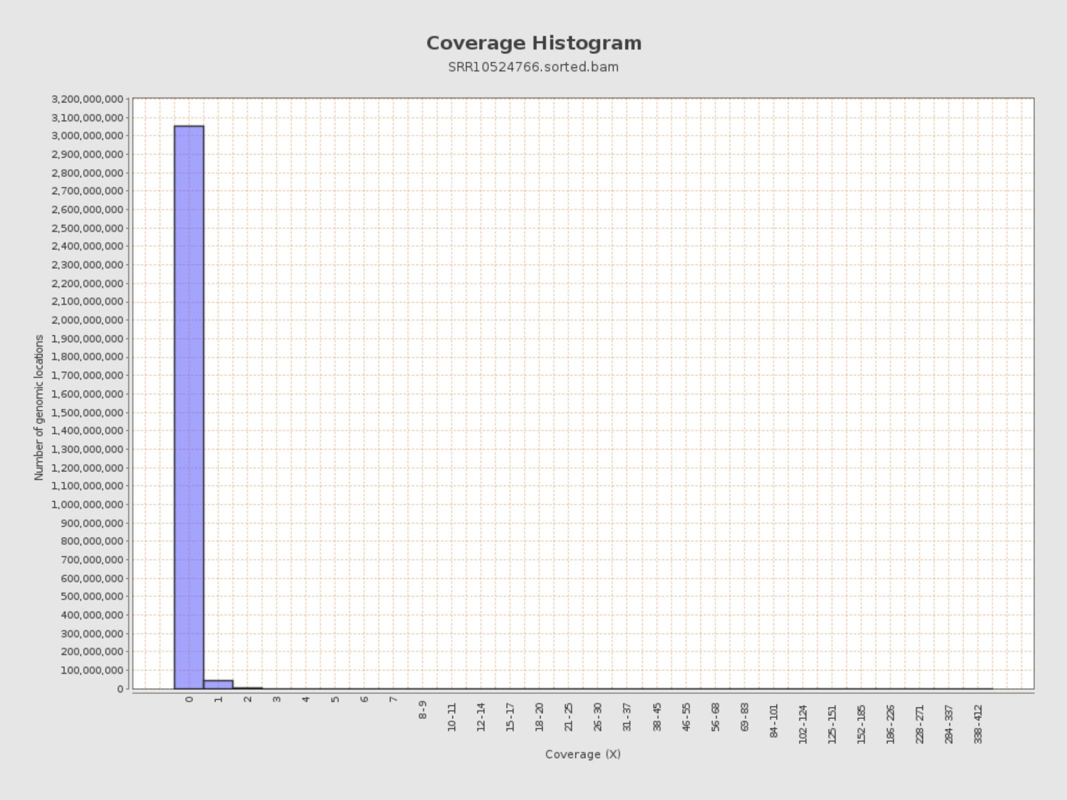
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5152668 | 0.0207 | 0.3102 |
| chr2 | 243199373 | 4041558 | 0.0166 | 0.2141 |
| chr3 | 198022430 | 3854751 | 0.0195 | 0.1462 |
| chr4 | 191154276 | 2792291 | 0.0146 | 0.1307 |
| chr5 | 180915260 | 2182791 | 0.0121 | 0.1146 |
| chr6 | 171115067 | 2437209 | 0.0142 | 0.1344 |
| chr7 | 159138663 | 2827583 | 0.0178 | 0.2286 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2259589 | 0.0154 | 0.1722 |
| chr9 | 141213431 | 1568930 | 0.0111 | 0.1306 |
| chr10 | 135534747 | 2609349 | 0.0193 | 0.1833 |
| chr11 | 135006516 | 2215608 | 0.0164 | 0.1533 |
| chr12 | 133851895 | 2171620 | 0.0162 | 0.1344 |
| chr13 | 115169878 | 1528809 | 0.0133 | 0.1208 |
| chr14 | 107349540 | 1829710 | 0.017 | 0.1381 |
| chr15 | 102531392 | 1328473 | 0.013 | 0.1204 |
| chr16 | 90354753 | 1262394 | 0.014 | 0.1303 |
| chr17 | 81195210 | 936063 | 0.0115 | 0.114 |
| chr18 | 78077248 | 1048946 | 0.0134 | 0.215 |
| chr19 | 59128983 | 855104 | 0.0145 | 0.2101 |
| chr20 | 63025520 | 861315 | 0.0137 | 0.1233 |
| chr21 | 48129895 | 623904 | 0.013 | 0.1233 |
| chr22 | 51304566 | 380338 | 0.0074 | 0.0896 |
| chrMT | 16571 | 56946 | 3.4365 | 2.5734 |
| chrX | 155270560 | 2488641 | 0.016 | 0.1381 |
| chrY | 59373566 | 142465 | 0.0024 | 0.0829 |

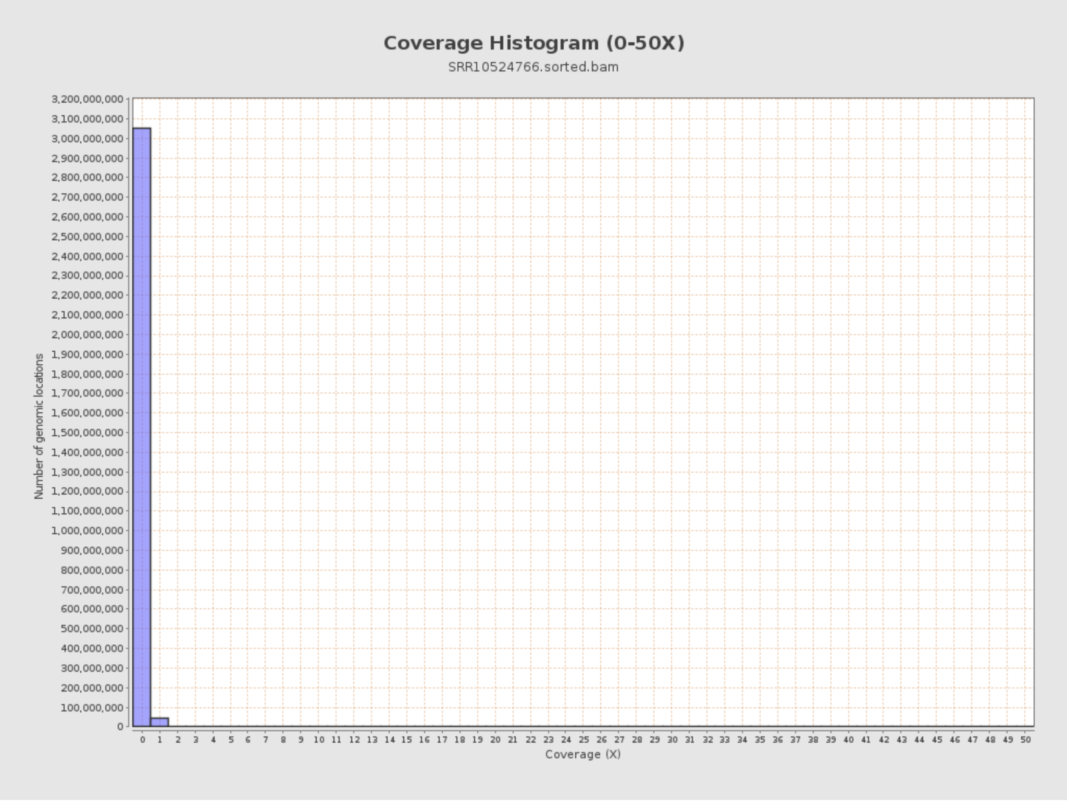
# 3. Results : Coverage across reference



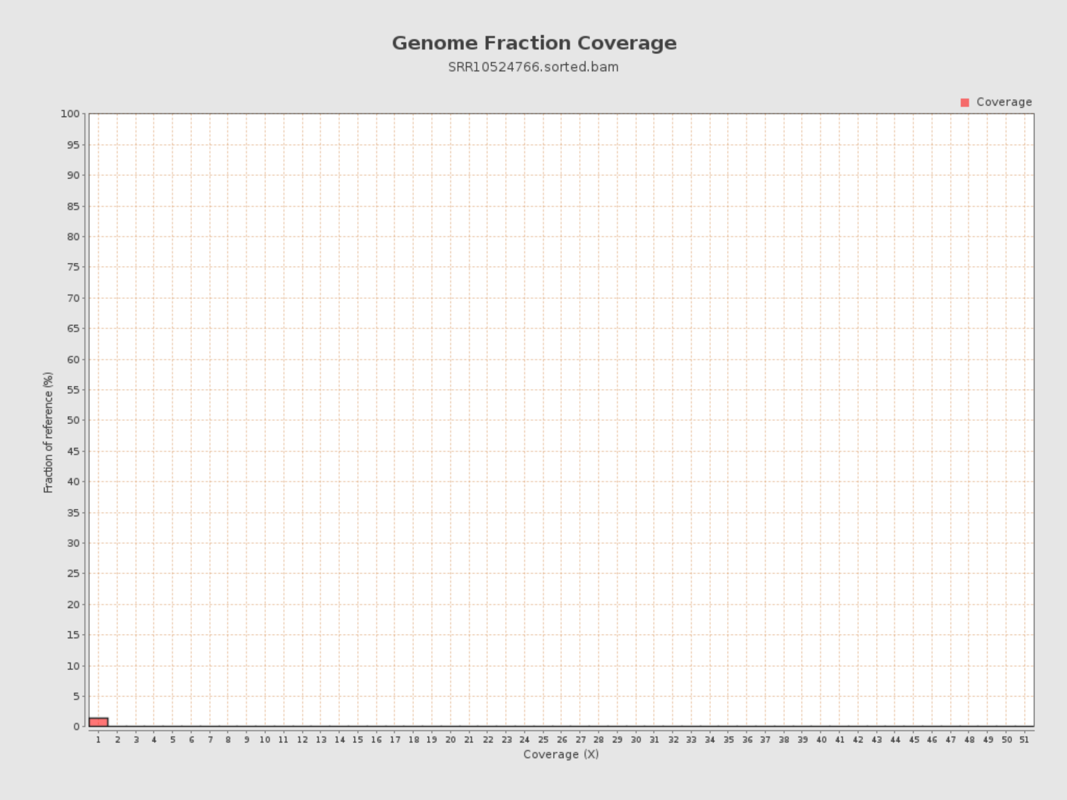
# 4. Results : Coverage Histogram



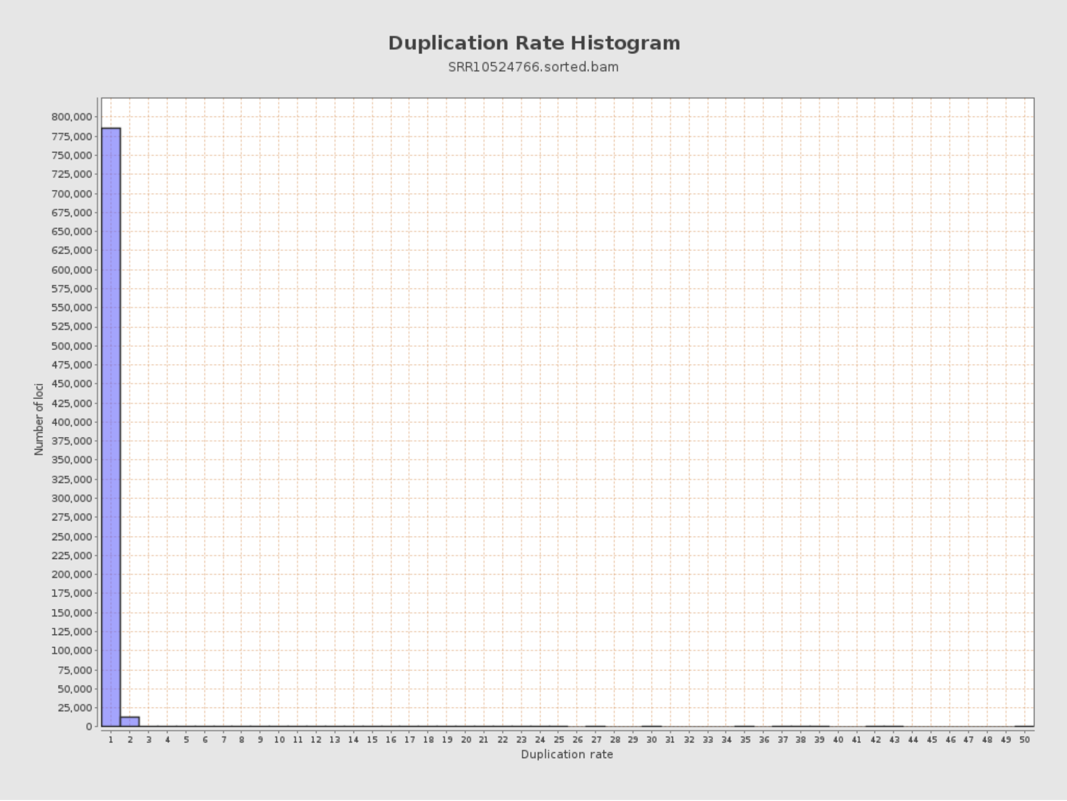
# 5. Results : Coverage Histogram (0-50X)



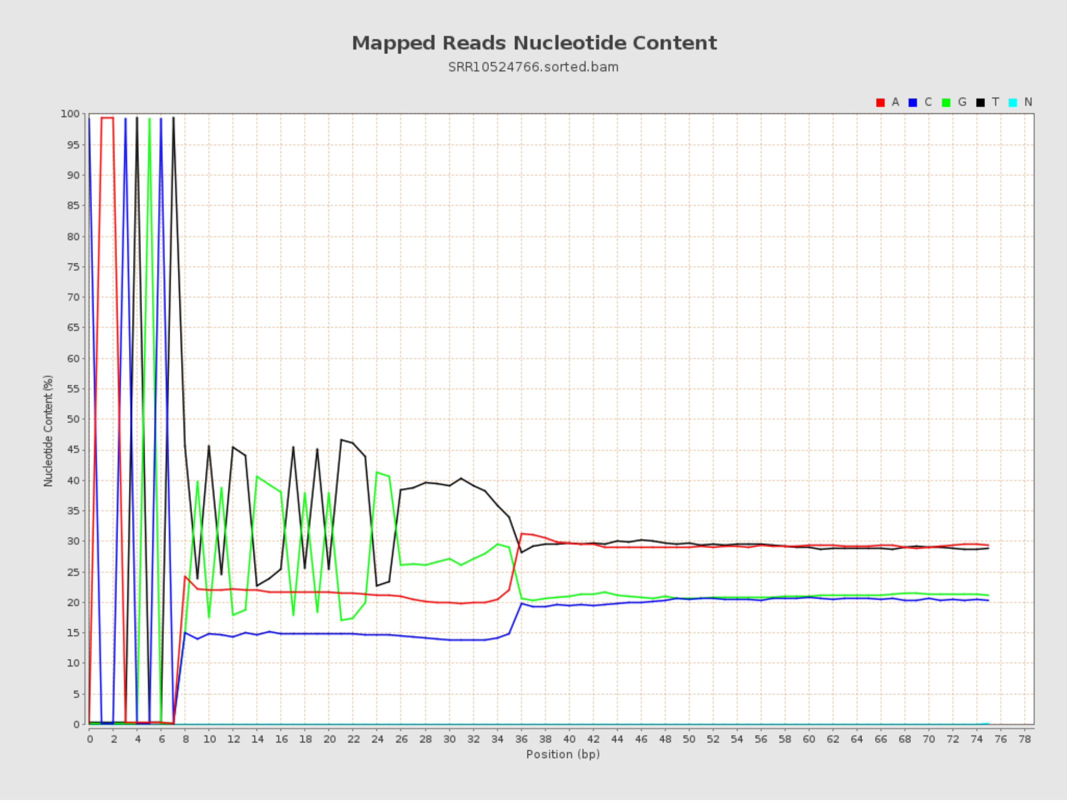
# 6. Results : Genome Fraction Coverage



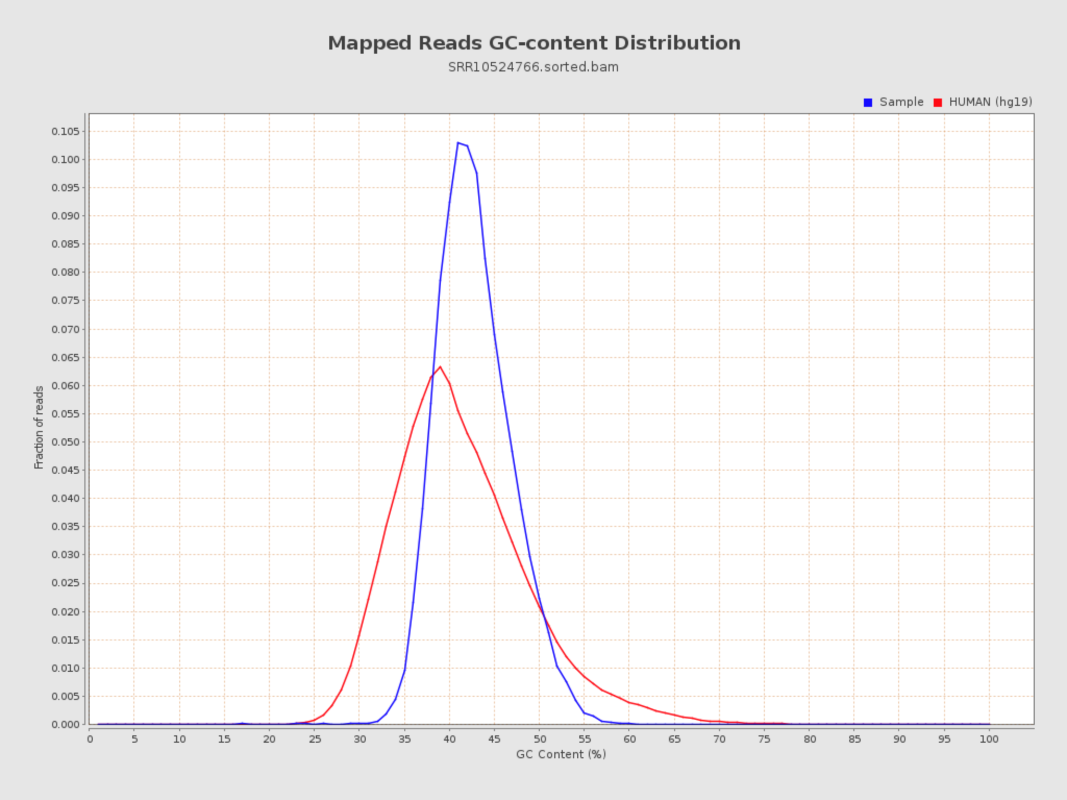
# 7. Results : Duplication Rate Histogram



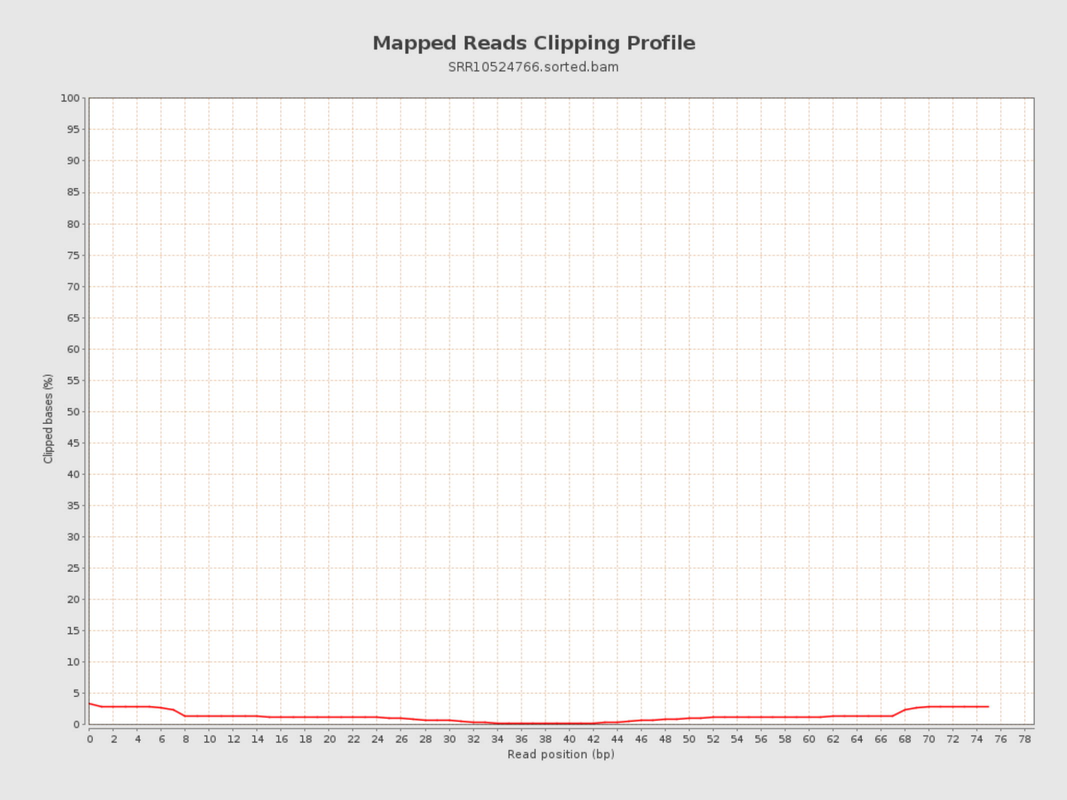
# 8. Results : Mapped Reads Nucleotide Content



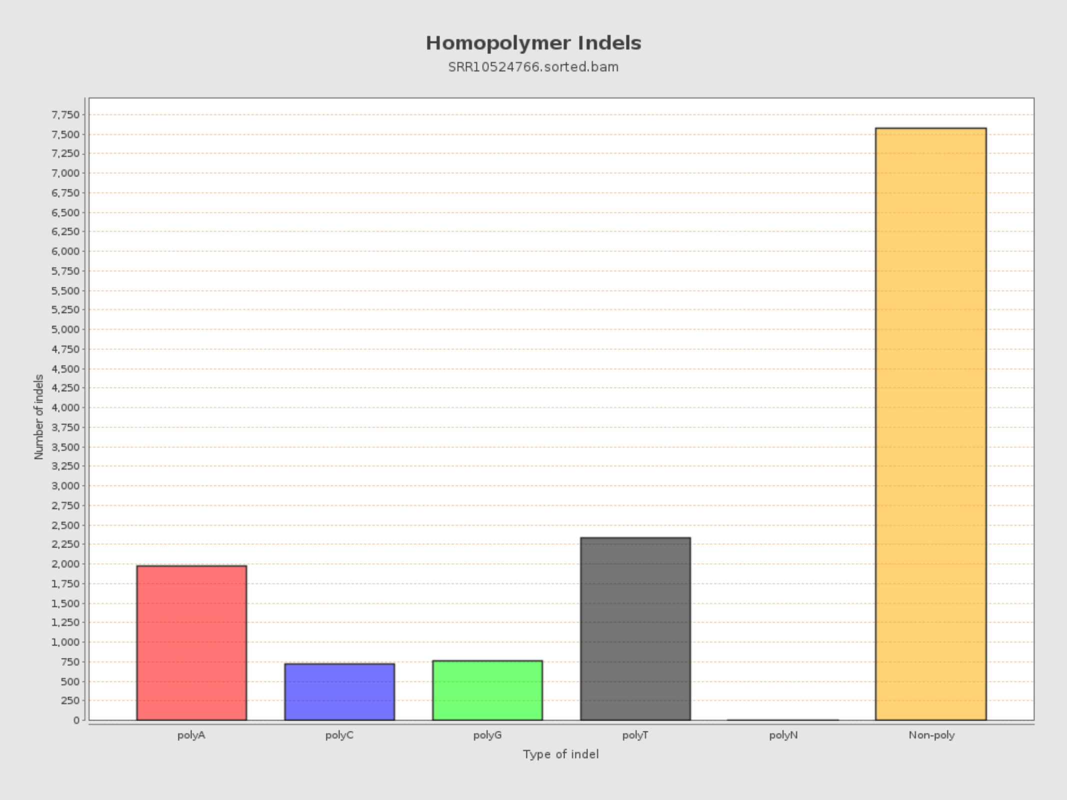
# 9. Results : Mapped Reads GC-content Distribution



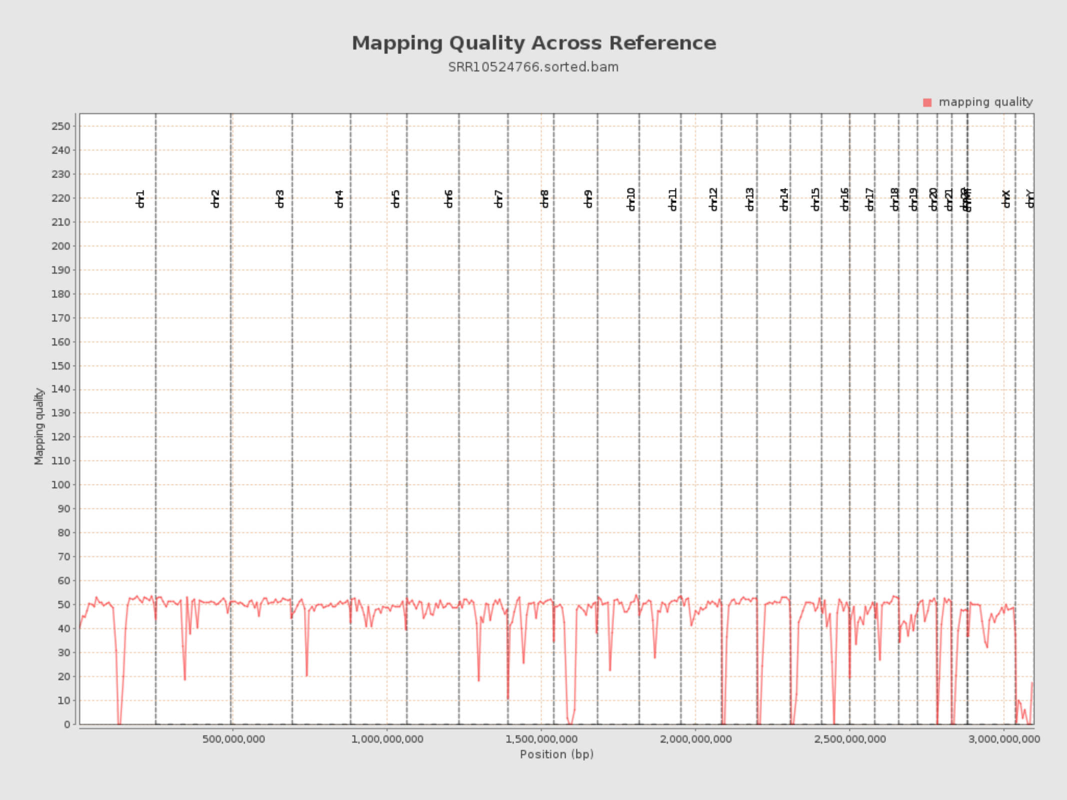
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram